

SEQ	ID	NO:	29	(gl 3080420)	
SEQ	ID	NO: 2			MSGAVLVAIAA
SEQ	ID	NO: 4			MGGAVMVAIAA
SEQ	ID	NO: 6			MAGAVLVAIAA
SEQ	ID	NO: 8			MKGAVLVAIAA
SEQ	ID	NO: 10			MSGAAALVAIAA
SEQ	ID	NO: 12			
SEQ	ID	NO: 14			
SEQ	ID	NO: 16			

SEQ	ID	NO:29	(gi 3080420)	61	120
SEQ	ID	NO:2		TCsggvadwlgrrpmlilssilyfvgslvmlwspnvyyvllgRLldgfgvglvvtlvpiy	
SEQ	ID	NO:4		TSpqpradcvgrpmlvasAVIYFVSGLVMLWAPIVYIILLARLldgfgiglavtlvpIy	
SEQ	ID	NO:6		-----	
SEQ	ID	NO:8		-----	
SEQ	ID	NO:10		tcsqpiadwlgrrpmmilssvlyflgglvmlwspnvyclarlldgfgiglavtlvpvy	
SEQ	ID	NO:12		-----	
SEQ	ID	NO:14		-----	
SEQ	ID	NO:16		-----	

SEQ	ID	NO:29	(gi 3080420)	121	180
SEQ	ID	NO:2		isetapp-eirGLLNTLPQFTG-SGGMFLSYCMVFGMSLMPSPSWRLMLGVLFIPSLVFF	
SEQ	ID	NO:4		isetaphrxswGXXNTLPQFIGVXGGMFLSYCMVFGMSLMPKPDWRLMLGVLSIPSLXYF	
SEQ	ID	NO:6		-----S---LI-----GAT-----I-----	
SEQ	ID	NO:8		isetaps-eirGSLNTLPQFSG-SGGMFLSYCMVFGMSLSPAPSWRLMLGVLSIPSLLYF	
SEQ	ID	NO:10		-----	
SEQ	ID	NO:12		-----	
SEQ	ID	NO:14		-----	
SEQ	ID	NO:16		-----	

FIG. 1A

SEQ ID NO:29	(gi 3080420)	181	FLTVFFLPESPRWLVS	KRMLEAKRVLQRLRGREDVSGEMALLVEGLGIGGETTIEEYII	240
SEQ ID NO:2			GLTVFYLPESPRWLVS	KGRMAEAKRVXQRLRGREDVSXEXALLVEGLGVGKDTRIXEYII	
SEQ ID NO:4			-----	-----IT-----TXS-----	
SEQ ID NO:6			-----	-----	
SEQ ID NO:8			ALTIFFLPESPRWLVS	KGRMLEAKKVLQRLRGREDVSGEMALLVEGLGIGGDTSEYII	
SEQ ID NO:10			-----	-----	
SEQ ID NO:12			-----	-----	
SEQ ID NO:14			-----	-----	
SEQ ID NO:16			-----	-----	
SEQ ID NO:29	(gi 3080420)	241	GPADVTDHDDIAVDKD-QIKLYGAEGLSWVARPVKG	-----GSTMSVLSRHGSTMSTRRQ	300
SEQ ID NO:2			GPATEAADDLVTDGDKE-QITLYGPEEGQSWIARPSKGPIMGLSVLSLARHGS-MVNQS	-----	
SEQ ID NO:4			-----	-----	
SEQ ID NO:6			-----	-----	
SEQ ID NO:8			GPADDVADGHEHATEKD-KIRLYGSQAGLSWLSKPVGTQ	-----SSIGLASHHGS-IINQS	
SEQ ID NO:10			-----DPSREKD-QIKLYGPEQGQSWVARPVAGP	-----NSVGLVSRKGS-MANPS	
SEQ ID NO:12			-----S-----	-----	
SEQ ID NO:14			-----	-----	
SEQ ID NO:16			-----	-----	
SEQ ID NO:29	(gi 3080420)	301	GSLIDPLVTLFGSVHEKMPDTG	-----SMRSALFPFHGSMFVS VGN--QPRHEDWD--EEN	360
SEQ ID NO:2			VPLMDPIVTLFGSVHENMPQAG	-----GSMRSTLFPNFGSMFVSVDQ--HAKNEQWD--EEN	
SEQ ID NO:4			-----	-----	
SEQ ID NO:6			-----	-----	
SEQ ID NO:8			MPLMDPLVTLFGSIHEKLPETGARGSMRSTLFPNFGSMFSTAE	-----PHAKIEQW--EES	
SEQ ID NO:10			-----SLVDPLVTLFGSVHEKLPETG	-----STLFPFHGSMFVS VGG--NQPRNEDWD--EES	
SEQ ID NO:12			-----	-----	
SEQ ID NO:14			-----	-----	
SEQ ID NO:16			-----	-----WK--E--	

FIG. 1B

SEQ ID NO:29	(gi 3080420)	361	LVGEGEDYPSD----	HGDDSEDDLHSP	LISRQTTSM	E-KDMPHTAH--	420	CTLSTFRHGSQV
SEQ ID NO:2			LHRDDEEYASD----	GAGDYEDNLHSP	LLSRQATGA	EKGDIVHHGR	GSALSMRRQS--	L
SEQ ID NO:4			-----	-----	-----	-----	-----	-----
SEQ ID NO:6			-----	-----	-----	-----	-----	-----
SEQ ID NO:8			-----	-----	-----	-----	-----	-----
SEQ ID NO:10			LQREDYMSDATRG---	DSDDNLHSP	LISRQTTSL	E-KDLPPF	SHGSI	LGSMRRHSSL
SEQ ID NO:12			LAREGDDYVSDA--G---	DSDDNLQSP	LISRQTTSL	D-KDIPPHA	H--SNLAS	MRQGSLL
SEQ ID NO:14			-----	-----	-----	-----	-----	-----
SEQ ID NO:16			-----	-----	-----	-----	-----	-----

SEQ ID NO:29	(gi 3080420)	421	QGAQGEAGSMGIGGWQ	VAWKWTERE	DESGQKEGF	-----	480	PGSRRGSI
SEQ ID NO:2			LGEGGDVSSTDIGGGWQ	LAWKWKSEKE	GENGRKEG	FKRVLHQEG	VP	GSRRGSI
SEQ ID NO:4			-----	-----	-----	-----	-----	-----
SEQ ID NO:6			-----	-----	-----	-----	-----	-----
SEQ ID NO:8			-----	-----	-----	-----	-----	-----
SEQ ID NO:10			MQSGEQGGSTGIGGWQ	LAWKWKTDK-	GEDGKQQGG	FKRIYLHEG	VSASRRG	SI
SEQ ID NO:12			HGNSGEPTGSTGIGGWQ	LAWKWKSERE	GPDKKEG	FKRIYLHQD	GGSGRRG	SVVSLPG
SEQ ID NO:14			-----	-----	-----	-----	-----	-----
SEQ ID NO:16			---GGEAVSSTGIGGWQ	LAWKWKSERQ	GEDGKKEG	FKRIYLHQE	GVADSR	RGSVVSLPG
			-----	-----	-----	-----	-----	-----

SEQ ID NO:29	(gi 3080420)	481	GDGTGEA--DFVQASAL	VSQPALYSK	DLLKEHT-	IGPAMVHP	SE-TTKG	SIWHD
SEQ ID NO:2			GGDVLEGS-EFVHAAAL	VSQSALFSK	GLAEPRM-	SDAAMVHP	SEVA	AKGSRWKDL
SEQ ID NO:4			-----	-----	-----	-----	-----	-----
SEQ ID NO:6			-----	-----	-----	-----	-----	-----
SEQ ID NO:8			EG-----EFVQAAAL	VSQPALYSK	ELIDGH-	PVGPAMVHP	SETA	SKGPSWKAL
SEQ ID NO:10			GDLPTD--SEVVQAAAL	VSQPALYNED	LMRQR-	PVGPAMVHP	SETI	AKGPSWSDL
SEQ ID NO:12			-----	-----	-----	-----	-----	-----
SEQ ID NO:14			GGDATQGGSGFIHAAAL	VSHSALYSK	DLMEERMA	AGPAMVHP	LEA	PKGSIWKDL
SEQ ID NO:16			-----	-----	-----	-----	-----	-----
			-----	-----	-----	-----	-----	EPGV

FIG. 1C

SEQ ID NO:29	(gi 3080420)	541	KRALVVGVLQILQQFSGINGVLYYTPQILEQAGVGILLNMGISSSASILISALTTFV	600
SEQ ID NO:2			RRALLVGVGIQILQQFAGINGVLYYTPQILEQAGVAVILSKFGLSSASAILISLTTLL	
SEQ ID NO:4			-----VL-----	
SEQ ID NO:6			KHALVVGVIQILQQFSGINGVLYYTPQILEEAGVEVLLSDIGIGSESASFLLISAFITFL	
SEQ ID NO:8			KHALIVGVMQILQQFSGINGVLYYTPQILEQAGVGILLSSGLGSTSSSFLISAVTTLL	
SEQ ID NO:10			RRALFVGVIQMLQQFAGINGVLYYTPQILEQAGVAVLLSNLGLSSASAILISLTTLL	
SEQ ID NO:12			KHALFVGIGLQILQQFAGINGVLYYTPQILEQAGVGVLNIGLSSSSASILISALTLL	
SEQ ID NO:14			601	
SEQ ID NO:16			MLPAIAVAMRLMDLSGRRLLLTIPILIASLLVLVISNLVHMNSIVHAVLSTVSVVLYF	660
			MLPCIGFAMLLMDLSGRRFLLLTIPILIASLVILVSNLIDLGLTAHALSTISVIVYF	
			-----TLILVNILDVGTVMVHASLSTVSVILYF	
			MLPCIGVAMKLMDSGRRQLLTIPVLIVSLIILVIGSLVNEGNVAHAAISTVCVVVYF	
			MLPCIAIAMRLMDISGRRLLLTIPVLIAALLILVGLSLVDLGSTANASISTISVIVYF	
			MLPSIGVAMRLMDISGRRFLLLTIPILIASLIVLGVNVNINLSTVPHAVLSTVSVIVYF	
			MLPSIGIAMRLMDMSGRRFLLLTIPVLIVALAVLVNVLVDVGTVMVHAALSTISVIVYF	
			661	
SEQ ID NO:29	(gi 3080420)		CCFVMGFGPAPNILCSEIFPTRVRGICIAICALTFWICDIIIVTYSPLPVLLKSI GLAGVFG	720
SEQ ID NO:2			CCFVMGFGPIPNILCAEIFPTRVRGLCIACAFTWIGDIIIVTYSPLPVMNAIGLAGVFS	
SEQ ID NO:4			-----	
SEQ ID NO:6			CCFVMGFGPIPNILCAEIFPTRVRGICIAICALTFWIGDIIIVTYSPLPVMNAIGLAGVFG	
SEQ ID NO:8			CCFVMGYGPIPNILCSEIFPTRVRGLCIAICALVFWIGDIIITYSPLPVMGLSLGGLGVFA	
SEQ ID NO:10			CCFVMGFGPIPNILCAEIFPTRVRGLCIAICALTFWICDIIIVTYSPLPVMNSVGLAGVFG	
SEQ ID NO:12			-----	
SEQ ID NO:14			CCFVMGFGPIPNILCAEIFPTRVRGVCAICALTFWICDIIIVTYSPLPVMNAIGLAGVFG	
SEQ ID NO:16			CCFVMGFGPIPNILCAEIFPTSVRGICIAICALTFWIGDIIIVTYSPLPVMNAIGLAGVFG	

FIG. 1D

SEQ ID NO: 29	(gi 3080420)	721	MYAIVCCISWVFVFIKVPETKGMPL	767
SEQ ID NO: 2			EVITEFFSVGARQAEA	--KNE
SEQ ID NO: 4			IYAVVCLISFVFLKVPETKGMPL	EVITEFFAVGAKQAAA
SEQ ID NO: 6			-----	-----KA
SEQ ID NO: 8			IYAVVCILAFVFMKVPETKGMPL	EVITEFFSVGAKQ-AKE
SEQ ID NO: 10			IYAVVCFISWIFVFLKVPETKGMPL	EVISEFFSVGAKQAASA
SEQ ID NO: 12			IYAVVCFIAWVFLKVPETKGMPL	EVIIIEFFSVGAKQFDDA
SEQ ID NO: 14			-----	-----KHN
SEQ ID NO: 16			IYAVVCCIAFVFVYLKVPETKGMPL	EVITEFFAVGAKQ-AQA
			IYAIVCVLA FVFVYMKVPETKGMPL	EVITEFFSVGAKQ-GKE
				---ATD

FIG. 1E

SEQ ID NO: 30
SEQ ID NO: 18
SEQ ID NO: 20
SEQ ID NO: 22
SEQ ID NO: 24
SEQ ID NO: 26
SEQ ID NO: 28

1 MSEG-----TNKAMSDPPPTTASKVIA--DF-DPLKKPPKRN---KFAFACAT 60
SR-----AQSEPSTMASA--PL--PAAIEPGKKGNVKKFAFACXI
M-----ASD--ELAK--AVEPRKKGNVKYASICAI
MTEG-----MASA--AL--PEAVAPKKKGNVRFACACAI
-----KLVAAEAH-----KTLQ--DF-DPPKKR-KRN---KYAFACAM
MKMS-----MDRA--AL--PAAVEPKKKGNVRFACACAI
-----PERKGAEDKEEGSRMASA--ALPEPGAVHPRNKGNEKYAFTCAL

SEQ ID NO: 30
SEQ ID NO: 18
SEQ ID NO: 20
SEQ ID NO: 22
SEQ ID NO: 24
SEQ ID NO: 26
SEQ ID NO: 28

61 LASMTSVLLGY-----DIGVMSGAIYILKEDWHISDTQIGVLVG 120
LASMTSILLGY-----DIGVMSGASLYIKKDLKISDVKLEILMG
LASMASVILGY-----DIGVMSGAAAMYIKKDLNITDVQLEILIG
LASMTSILLGY-----DIGVMSGASLYIKKDFNISDGKVEVLVG
LASMTSILLGY-----DIGVMSGAAIYIKRDLKVSDEQIEILLG
CASMATIVLGY-----DVGVMMSGASLYIKRDLQITDVQLEIMMG

SEQ ID NO: 30
SEQ ID NO: 18
SEQ ID NO: 20
SEQ ID NO: 22
SEQ ID NO: 24
SEQ ID NO: 26
SEQ ID NO: 28

121 ILNIYCLFGSFAAGRTSDWIGRRYTIVLAGAIEFVGALLMGFATNYAFMLVGRFVTGIGV 180
ILNVYSLIGSXAAGRTSDWIGRRXTIVEAAVIEFAGAXLMGFVAVNYWMLMFGRFVAGIGV
ILSLYSLFGSFAAGRTSDRIGRRRLTVVFAAVIEFVGSLLMGFAVNYGMLMAGRFVAGVGV
ILNLVSLIGSFAAGRTSDWIGRRYTIVEAAVIEFAGXFLMGFAVNYAMLMEGRFVAGIGV
IINLYSLIGSCLAGRTSDWIGPRYTIVEAGTIEFVGALLMGFSPNYSFLMEGRFVAGIGI
ILNVYSLIGSFAAGRTSDWIGRRFTIVEAAVIEFAGALIMGFSVNYAMLMEGRFVAGIGV
ILSVYALIGSFLGARTSDWVGRRVTVVEAAAIENNGSLLMGFAVNYAMLVGRFVTGIGV

FIG. 2A

SEQ ID NO:30	181	GYALMIAPVYTAEVSPASSRGFLTSFPEVF	240
SEQ ID NO:18		GYALMIATVYTAEVSPXSARGFLTSFPEVFI	
SEQ ID NO:20		GYGGMIAPVYTAEISPAASRGFLTTFPEVF	
SEQ ID NO:22		GYALMIAPVYTAEVSPASARGFLTSFPEVF	
SEQ ID NO:24		GYALMIAPVYTAEVSPASSRGFLTSFPEVF	
SEQ ID NO:26		GYALMIAPVNTGEVSPASARGVLTSPPEVF	
SEQ ID NO:28		GYAIMVAPVYTPEVSPASARGFLTSFTEVF	
		INVGILLGYVSNYAFARLPLHLHLSWRV	
		MLGI	
SEQ ID NO:30	300	GAIPSI FLAIGVLAMPESPRWLVMQGR	
SEQ ID NO:18		LDGDAKKVLNRISDSPEEAQLRLSEIKQ	
SEQ ID NO:20		TAGIPA	
SEQ ID NO:22		GAVPSGLLALLVFCMPESPRWLVLKGR	
SEQ ID NO:24		LADARAVLEKTSATPEEAERLADIKAA	
SEQ ID NO:26		AGIPK	
SEQ ID NO:28		GAAPSVLLALMVLGMPESPRWLVMKGR	
		LADAKVVLEKTSDTAEAAERLADIKAA	
		AGIPE	
		GAIPSVLLTVGVLAMPESPRWLVMRGR	
		LGEARKVLNKTSDSKEEAQLRLAEIKQ	
		AAAGIPE	
		GAVPSVLLAFMVLGMPESPRWLVMKGR	
		LADAKVVLAKTSDTPEEAAERLADIKT	
		AAAGIPL	
		GAVPSALLALMVFGMPESPRWLVMKGR	
		LADARAVLAKTSDTPEEAVERLDQIKAA	
		AGIPR	
SEQ ID NO:30	360	ECDEDIYKVEKTKIKSGNA-VWKELFF	
SEQ ID NO:18		NPTPAVRRAVIAGIGIHFFQQASGIDAV	
SEQ ID NO:20		VLYSP	
SEQ ID NO:22		GLDGDVVTVPGEQGGELQVWKKLILSPT	
SEQ ID NO:24		PAVRRILLSAVGLHFFQQASGSDSVVQY	
SEQ ID NO:26		SA	
SEQ ID NO:28		ELDGDVVTVPK-RGSGNEKRVWKELILSPT	
		PAMRRILLSGIGIHFFQHALGHSVVFYSP	
		SCNDDVVQVKNQS--NGEG-VWKELFLYPT	
		PAIRHIVIAALGIGHFFQQASGVDVAVVLYSP	
		GLDGDVVPVPKNKGSSEKRVLKDILSPT	
		IAMRHILIAIGIGIHFFQQSSGIDAVVLYSP	
		ELDGDVVVMP-KTKGGQEKQVWKELIFSPT	
		PAMRRILLALGIGHFFQQATGSDSVVLYSP	

FIG. 2B

SEQ ID NO:30	361	RIFQSAGITNARKQLLATVAVGVVKTFLFILVATFQLDKYGRRPRLLLTSVGGMIILTLA	420
SEQ ID NO:18		-----	
SEQ ID NO:20		RLFKSAGITDDNKL LGVTC AVGVTKTFFILVATFLLDRAGRRPRLLLISTGGMIVSLICLG	
SEQ ID NO:22		LVFKSPGLTNDKHFELGTTWPEFVTKRLEFILLATFFIDGVGRRPRLLLGSTGGIILSLIGLG	
SEQ ID NO:24		RIFEKAGITNDTHKLLATVAVGVFVKTVEILAATFTLDRVGRRPRLLLSSVGMVLSLLTLA	
SEQ ID NO:26		LVFKSAGITGDSRLRGTTVAVGATNTVFILVATFLLDRIRRRPRLVLTSTGGMLVSLVGLA	
SEQ ID NO:28		RVFQSAGITGDNHLLGATCAMGVMTLFIILVATFQLDRVGRRPRLLLTSTAGMLACLIGLG	
SEQ ID NO:30	421	MSLTVID-HSHHKITWAIALCITMVCVVAVSESIGLGPITWVYSSEVFPLRLRAQQTSMG	480
SEQ ID NO:18		-----	
SEQ ID NO:20		SGLTVAGHHPDTKVAVAVALCIASLSYIAFFSIGLGPITGVYTSEIFPLQVRALGFAVG	
SEQ ID NO:22		AGLTVVGQHPDAKI PWAIGLSIASTLAYVAFFSIGLGPITWVYSSEIFPLQVRALGCSLG	
SEQ ID NO:24		ISLTVID-HSERKLMWAVGSSIAMVLAYVATFSIGAGPITWVYSSEIFPLRLRAQQAAG	
SEQ ID NO:26		TGLTVISRHPDEKITWAIVLCIFCIMAYVAFFSIGLGPITWVYSSEIFPLHVRALGCSLG	
SEQ ID NO:28		TGLTVVGRHPDAKVPWAIGLCIVSILAYVSFFSIGLGPLTSVYTSSEVFPLRVRALGFALG	
SEQ ID NO:30	481	VAVNRVVGVISIFFLPLSHKITTGGAFFLFGGIAIAWFFFLTPETRGRTLENMHIEL	540
SEQ ID NO:18		-----	
SEQ ID NO:20		VASNRVTSAVISMTFLSLSKAITIGGSFFLYSGIAAVAVVFFFTCLPETRGRTLEEMGKL	
SEQ ID NO:22		VANRVTSGVISMTFLSLSKAITIGGSFFLYSGIAALAWVFFFTYLPETRGRTLEEMSKL	
SEQ ID NO:24		VAVNRVTSVAVVSMTEFLSLTRAITIGGAFFLYCGIATVGWIFFFTYLPETRGKTLEDMEGS	
SEQ ID NO:26		VAVNRVTSVAVVSMTEFLSLSKAMTIGGAFFLFAGIASFAWVFFFTYLPETRGKTLEDMSSL	
SEQ ID NO:28		TSCNRVTSAAVSMTEFLSLSKAITIGGSFFLYAGIAAGWIFFFTYLPETRGKPLEEIGKL	

FIG. 2C

SEQ ID NO:30
SEQ ID NO:18
SEQ ID NO:20
SEQ ID NO:22
SEQ ID NO:24
SEQ ID NO:26
SEQ ID NO:28

541
FEDFRWRESFPGNKSNNDENSTRKQSNQNDKQVQLGETTSTTVTNDNH

FGM-----PDTGMAEEAEDA-AAKEKVVELPSSK-----TS-----
FGD-----TAAASESEPAKEK---KKVEMAATN-----
FGTFRSKSN--ASKAVENENG-----QVAQVQLG-----TNVQT
FGN-----TATHKQGAEEADDDAGEKKVEMAATN-----
FGM-----TDTAVEAQDTAT-KDKAKVGEM---N-----

590

FIG. 2D